Amendment to the Specification

Please replace the paragraph beginning at page 6, line 18 with the following rewritten paragraph:

Fig. 3 shows PCR primers SEQ ID NOS: 1-25 and 27-28 used to PCR amplify and/or sequence the approximately 10 kb nucleic acid region that is 5′ upstream of the chicken ovomucoid transcription start site.

Please replace the paragraph beginning at page 15, line 24 with the following rewritten paragraph:

The terms "percent sequence identity" or "percent sequence similarity" as used herein refer to the degree of sequence identity between two nucleic acid sequences or two amino acid sequences as determined using the algorithm of Karlin and Attschul 1990 *Proc. Natl. Acad. Sci.* 87: 2264-2268, modified as in Karlin and Attschul 1993 *Proc. Natl. Acad. Sci.* 90: 5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Attschul et al. 1990 *T. Mol. Biol.* Q15: 403-410. BLAST nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleic acid molecule of the invention. BLAST protein searches are performed with the XBLAST program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to a reference polypeptide. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Attschul et al. 1997 *Nucl. Acids Res.* 25: 3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g. XBLAST and NBLAST) are used. ~~See http://www.ncbi.nlm.nih.gov~~. Other algorithms, programs and default settings may also be suitable such as, but not only, the GCG-Sequence Analysis Package of the U.K. Human Genome Mapping Project Resource Centre that includes programs for nucleotide or amino acid sequence comparisons.